

SEQUENCE LISTING



<110> TransMIT Gesellschaft für Technologietransfer mbH
TransMIT Gesellschaft für Technologietransfer mbH

<120> Method for screening the allelic state at the 5'-flanking region of the
aS1 casein gene

<130> An127/Pri

<140> PCT/DE 03/02747

<141> 2003-08-15

<150> DE 102 38 433 A1

<151> 2002-08-16

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> DNA

<213> Bos spec.

<220>

<221> Primer 2

<222> (1)..(18)

<223> 18 basepair, single stranded nucleic acid (linear)

<400> 1
gaagaagcag caagctgg

<210> 2

<211> 19

<212> DNA

<213> Bos spec.

<220>

<221> Primer 3

<222> (1)..(19)

<223> 19 basepair, single stranded nucleic acid (linear)

<400> 2

ccttgaaata ttctaccag

19

<210> 3

<211> 1061

<212> DNA

<213> Bos taurus

<220>

<221> alpha-S1Kaseingen

<222> (1)..(1061)

<223> start Exon 1 at position 620

<300>

<301> Koczan Dirk, Hobom Gerd, Seyfert Hans-Martin

<302> Genomic organization of the bovine alpha S1-casein gene

<303> Nucleic acids research

<304> 19

<305> 20

<306> 5591

<307> 1991-09-24

<308> X59856

<309> 1991-07-18

<313> (1) .. (1061)

<300>

<308> EMBL X59856

<309> 1991-07-18

<313> (1) .. (1061)

<400> 3

gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg	60
gtataattaa aatgccacca aaattttatac aataattata ttttcttttt gcaggaaaaa	120
gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg	180
gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt	240
aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat	300
tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa	360
taaccataaa tctaggggtt tgttgggggt tttttttgtt tgttaattta gaacaatgcc	420
attccatttc ctgtataatg agtcacttct ttgttgtaaa ctctccttag aatttcttgg	480
gagaggaact gaacagaaca ttgatttcct atgtgagaga attcttagaa tttaaataaa	540
cctgttggtt aaactgaaac cacaaaatta gcattttact aatcagtagg tttaaatagc	600
ttggaagcaa aagtctgcca tcaccttgat catcaaccca gcttgctgct tcttcccagt	660
cttgggttca aggtattatg tatacatata acaaaatttc tatgattttc ctctgtctca	720
tctttcattc ttcactaata cgcagttgta acttttctat gtgattgcaa gtattggtac	780
tttcctatga tatactgtta gcttaaaaat atatttgcaa atgttgatac tatctatctc	840
agagctatag gtgaaaaatt aaatactttt ataaagacca aattgatcat ttttaaacga	900
aattcttata tactgaaaat gtagatacat aacttcagta tagatttatg gtaaaataat	960
ttgaatcatt tttgtcaaat tctgtaaaaa gttgtcatac agaataattt ataataattt	1020
tgttttcata gaaataacat ttctggtaga atatttcaag g	1061

<210> 4

<211> 652

<212> DNA

<213> Bos taurus

<220>

<221> CSN1S1-gene, 5`flanking region from position 616 and Exon 1 at position 617

<222> (1)..(652)

<223> Mutation/SNP position 83 (A to G), position 98 (A to G), position 298 (A to C), position 442 (A to G; change/loss of YY1- and AP1 -bindingsite), position 541 (G to A); deletion TT between position 389 and 394 compaired with Allel2

<400> 4

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gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60
gtataattaa aatgccacca aagtttatac aataattgta ttttcttttt gcaggaaaaa     120
gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataaatatg     180
gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt      240
aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcct ttacaggtat      300
tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa     360
taaccataaa tctagggttt tgttgggggt ttttgtttgt taatttagaa caatgccatt      420
ccatttcctg tataatgagt cgcttctttg ttgtaaactc tccttagaat ttcttgggag      480
aggaactgaa cagaacattg atttcctatg tgagagaatt cttagaattt aaataaacct      540
attgggttaa ctgaaaccac aaaattagca ttttactaat cagtaggttt aaatagcttg      600
gaagcaaaag tctgcatca ccttgatcat caaccagct tgctgctttc tt                652
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<210> 5

<211> 654

<212> DNA

<213> Bos taurus

<220>

<221> CSN1S1-gene, 5`flanking region and Exon 1

<222> (1)..(654)

<223> Bindingsite for transcriptionfactor AP-1 at position 438 to 445
Bindingsite for transcriptionfactor YY-1 at position 443 to 448

<400> 5

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gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg      60
gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa     120
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gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg	180
gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggg cttgtatggt	240
aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat	300
tgaatttttc aaagggtaca aaggaaattt tattgatata ataaatgcat gttctcataa	360
taaccataaa tctaggggtt tgttgggggt ttttttggtt gttaatttag aacaatgcca	420
ttccatttcc tgtataatga gtcacttctt tggtgtaaac tctccttaga atttcttggg	480
agaggaactg aacagaacat tgatttccta tgtgagagaa ttcttagaat ttaaataaac	540
ctggttggtta aactgaaacc acaaaatttag cattttacta atcagtaggt ttaaataagct	600
tggaagcaaa agtctgccat caccttgatc atcaaccag cttgctgctt tctt	654

<210> 6

<211> 650

<212> DNA

<213> Bos taurus

<220>

<221> CSN1S1-gene, 5`flanking region

<222> (1) .. (650)

<223> Bindingsite for transcriptionfactor AP-1 at position 434 to 441
 Bindingsite for transcriptionfactor YY-1 at position 439 to 444
 deletion G and TTT between 390 and 396 compaired with Allel 2

<400> 6

gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg	60
gtataattaa aatgccacca aaattttatac aataattata ttttcttttt gcaggaaaaa	120
gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg	180
gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggg cttgtatggt	240
aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat	300
tgaatttttc aaagggtaca aaggaaattt tattgatata ataaatgcat gttctcataa	360
taaccataaa tctaggggtt tgttgggggt ttttttggtt atttagaaca atgccattcc	420
atttcttgta taatgagtca cttctttggt gtaaaactct cttagaattt cttgggagag	480
gaactgaaca gaacattgat ttcttatgtg agagaattct tagaatttaa ataaacctgt	540
tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttta atagcttgga	600

agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt

650

<210> 7

<211> 650

<212> DNA

<213> Bos taurus

<220>

<221> CSN1S1-gene, 5`flanking region

<222> (1)..(650)

<223> Bindingsite for transcriptionfactors: AP-1 at position 434 to 441
, ABF1 at position 469 to 483, YY-1 at position 439 to 444;
mutation (SNP) at position 480 (G to C), developing a ABF1-bindin
g site;
deletion G and TTT between position 390 and 396 compaired with Al
lel 2

<400> 7

gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg	60
gtataattaa aatgccacca aaattttatac aataattata ttttcttttt gcaggaaaaa	120
gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg	180
gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatggt	240
aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacagggtat	300
tgaatttttc aaagggttaca aaggaaattt tattgatata ataaatgcat gttctcataa	360
taaccataaa tctagggttt tggtgggggt ttttttgta atttagaaca atgccattcc	420
atttcctgta taatgagtca cttctttggt gtaaactctc cttagaattt cttgggagac	480
gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt	540
tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga	600
agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt	650

<210> 8

<211> 20

<212> DNA

<213> Bos spec.

<220>

• • • •

• • • • • <221> Primer1

<222> (1)..(20)

<223> 20 basepair, single stranded nucleic acid (linear)

<400> 8

gaatgaatga actagttacc

20